

Antiviral strategies for hepatitis E virus

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ABSTRACT

The hepatitis E virus is a common cause of acute hepatitis. Contrary to hepatitis B and C, hepatitis E is mostly a mild infection, although it has a high mortality in pregnant women and can evolve to chronicity in immunocompromised patients. Ribavirin and pegylated interferon- α are the only available therapies, but both have side effects that are not acceptable for prophylaxis or treatment of mild infections. In addition, these drugs cannot be used for all patient types (e.g. in case of pregnancy, specific organ transplants or co-morbidities) and in resource-poor settings. Hence there is an urgent need for better antiviral treatments that are efficacious and safe, also during pregnancy. In this review, a concise introduction to the virus and disease is provided, followed by a discussion of the available assay systems and potential molecular targets (viral proteins and host factors) for the development of inhibitors of HEV replication. Finally, directions for future research are presented.

KEYWORDS

hepatitis E virus; antiviral therapy; inhibitor; host factor; ribavirin; interferon

1. INTRODUCTION

Hepatitis E virus (HEV) is a feco-orally transmitted pathogen and one of the most common causes of acute hepatitis worldwide. Although the virus was already identified in 1983 (Balayan et al., 1983), many of its epidemiological and clinical features are becoming clear just recently. HEV is responsible for both acute outbreaks in developing countries and sporadic cases worldwide and is more and more being recognized as a problem in the transplant setting (Kamar et al., 2008a; Pischke et al., 2012). Although most infections are self-resolving, hepatitis E is characterized by a high mortality in pregnant women and can lead to chronic infections in immunocompromised patients. A vaccine has recently been approved for the Chinese, but not for other markets (Zhu et al., 2010). Current therapeutic options (i.e. ribavirin and interferon- α) have severe side effects and treatment failure has been reported. It may be important to have potent and safe inhibitors of HEV replication at hand to rapidly contain outbreaks and to treat immunodeficient patients.

In this review, a general introduction to HEV is presented, followed by an overview of different potential antiviral targets and currently available methods for drug testing. Directions for developing antivirals against the HEV will be suggested.

2. HEPATITIS E VIRUS

a. Genome structure

HEV has a capped positive-sense single-stranded RNA genome that comprises a 5' untranslated region (UTR), open reading frames (ORF) 1 to 3 and a 3' UTR followed by a polyA-tract (see figure 1). ORF1 encodes the non-structural proteins and contains methyltransferase, protease, macrodomain, helicase and RNA-dependent RNA polymerase (RdRp)-encoding sequences (Koonin et al., 1992). Between the protease and the macrodomain, a hypervariable region containing a proline-rich hinge was found (Smith et al., 2012). The overlapping ORFs 2 and 3 are translated from a single subgenomic RNA into the structural proteins (Graff et al., 2006). ORF2 encodes the 660-aa capsid protein that consists of a shell domain (S), a middle domain (M, also called P1) and a protruding domain (P, also

called P2) (Guu et al., 2009; Yamashita et al., 2009). The protein translated from ORF3 is 114 aa in length, is phosphorylated (Zafrullah et al., 1997) and unique to HEV and closely related viruses.

b. Replication cycle

Although understudied, the HEV replication cycle seems typical for a single-stranded RNA virus of positive polarity (see figure 2). The virus particle first binds to heparan sulphate proteoglycans (HSPGs) on the host cell membrane (Kalia et al., 2009), transfers to its (unknown) cellular membrane receptor(s) and the resulting complex is internalized through clathrin-mediated endocytosis (Kapur et al., 2012). Consequently, the capped viral genome is released from the virion during the uncoating process and directly translated by the host cell ribosomal machinery. The non-structural proteins thus generated allow for the replication of the viral genome (probably in specific viral replication complexes) and the production of subgenomic RNA that is translated into the structural proteins from ORF2 and ORF3. Full-length RNA progeny is assembled with ORF2 capsid protein into viral particles of 27 to 30 nm (Balayan et al., 1983) that are consequently released from the cell in a non-lytic fashion. During release, HEV particles probably acquire a lipid bilayer (envelope) and associated ORF3 protein that are removed later by bile salts and enteric proteases respectively (Takahashi et al., 2010; Yamada et al., 2009).

c. Genetic diversity

HEV is classified into the *Hepevirus* genus in the family of the *Hepeviridae* (ref ICTV). At least 4 genotypes are currently recognized (Smith et al., 2013); genotypes 1 and 2 solely infect humans while genotypes 3 and 4 are zoonotic agents with their main reservoir in domestic pigs (Feagins et al., 2007; Meng et al., 1997; Tamada et al., 2004). Two additional genotypes have been proposed for HEV isolates from Japanese wild boars (Smith et al., 2013). Several viruses that are more or less related to HEV have been isolated from different species, including chickens (avian HEV, (Haqshenas et al., 2001)), rabbits (Zhao et al., 2009), rats (Johne et al., 2010), bats (Drexler et al., 2012), ferrets (Raj et al., 2012) and trout (Batts et al., 2011) (figure 3). The exact classification of these viruses

remains to be determined (Smith et al., 2013) and future discovery of additional hepeviruses seems likely.

3. HEPATITIS E

a. Epidemiology of disease

HEV genotypes 1 and 2 only infect humans and are endemic in many developing regions where they tend to cause large-scale water-borne outbreaks (Corwin et al., 1996; Naik et al., 1992). Genotype 1 is mainly found in Asia and Africa (Sugitani et al., 2009; Teshale et al., 2010), while genotype 2 has been isolated from Mexico and Africa, but seems less common (Maila et al., 2004; Velázquez et al., 1990) (see figure 4). It is estimated that infections with these genotypes result in 70,000 deaths annually (Rein et al., 2012). Genotypes 3 and 4 on the other hand are zoonotic agents with their main reservoir in domestic pigs (Colson et al., 2010; Li et al., 2005; Takahashi et al., 2004). Genotype 3 has a worldwide distribution, while genotype 4 is mostly found in Asia (Miyashita et al., 2012; Wang et al., 2012). However, genotype 4 has also been isolated from European pigs and patients recently (Hakze-van der Honing et al., 2011; Jebblaoui et al., 2013). Genotype 3 and 4 infections often result from consumption of undercooked pig or deer meat and may thus cause sporadic cases of hepatitis E. Although exact epidemiological data are missing, these infections seem a lot more common than initially thought (Dalton et al., 2008; Ijaz et al., 2009; Versluis et al., 2013).

b. Clinical syndromes

Acute hepatitis E is characterized by jaundice, fatigue, gastrointestinal discomfort etc. and is clinically indistinguishable from for instance hepatitis A (Khuroo, 1980), although many infections remain asymptomatic. Most cases of hepatitis E resolve spontaneously, but in some patients the infection may progress to fulminant hepatitis. Overall mortality rates are estimated between 0.5 and 4% (e.g. (Khuroo, 1980; Teshale et al., 2010)).

One particularly intriguing characteristic is that hepatitis E is often lethal in pregnant women with mortality rates of up to 20-25% (Khuroo et al., 1981; Tsega et al., 1993), although this has only been

observed for genotype 1 infections. Increased frequencies of obstetric complications and stillbirths have also been reported (Patra et al., 2007). The underlying mechanisms of this phenomenon (hormonal, immunological, genetical factors, etc.) are unclear to date.

A more recent finding is that HEV can establish chronic infections in immunocompromised subjects such as transplant and HIV-infected patients (Colson et al., 2009; Dalton et al., 2009; Kamar et al., 2008b). This has only been reported for genotype 3 thus far. Such chronic infections are rarely symptomatic and are sometimes mistaken for drug-induced liver injury (Davern et al., 2011). Chronic hepatitis E may lead to cirrhosis in 10% of patients (Kamar et al., 2011) and can ultimately result in death.

Occasional extrahepatic manifestations have also been reported; these are mostly neurological complications such as Guillain-Barré syndrome and neuralgic amyotrophy (Fong and Illahi, 2009; Kamar et al., 2010b; Sood et al., 2000) or nefrological manifestations such as glomerulonephritis (Kamar et al., 2012).

As evident from the discussion above, hepatitis E is profoundly different from the well-known disease courses of hepatitis B and C. While a considerable portion of patients infected with the hepatitis B virus (HBV) and especially the hepatitis C virus (HCV) evolves to chronicity, spontaneous recovery is the rule for hepatitis E where chronic disease has thus far only been reported in immunocompromised patients. The high rate of mortality in pregnant women is also unique to hepatitis E and no similar phenomena have been reported for hepatitis A, B or C.

c. Diagnostic methods

The most frequently used tests for diagnosing hepatitis E are detection of IgM and IgG antibodies by enzyme-linked immunosorbent assays (ELISA) and detection of viral RNA by (quantitative) reverse transcription PCR (RT-PCR). Presence of IgM antibodies indicates a recent infection, while IgG antibodies appear later and persist afterwards, at least for some time, indicating a past exposure. The current ELISAs suffer from large variability between assays (Bendall et al., 2010; Drobeniuc et al.,

2010; Mast et al., 1998) and therefore require urgent optimization and validation. Acute infection is usually confirmed by (quantitative) RT-PCR (e.g. (Jothikumar et al., 2006)), although these assays should be standardized as well to increase reliability.

Since the incubation and symptomatic periods for acute hepatitis E are only a few weeks, the successful use of antiviral drugs for acute cases of hepatitis E would depend on the availability of a rapid and inexpensive diagnostic test. Such test should also be easy to employ in resource-poor settings.

4. CURRENT CONTROL STRATEGIES

a. Vaccines

Vaccination would be an effective strategy to prevent HEV infection. Recently, such a HEV vaccine based on a recombinant truncated capsid protein was approved in China (Hecolin®, (Zhu et al., 2010)). It remains unclear whether the manufacturer intends to obtain market approval in other countries as well. Another recombinant vaccine successfully completed phase 2 clinical trials in Nepal (Shrestha et al., 2007), but further development was halted. Such vaccines may be useful as a prophylactic measure in high-risk patients such as immunocompromised patients and pregnant women. This would require specific clinical trials to demonstrate protective efficacy in these populations; to the best of our knowledge, such studies have not yet been reported for Hecolin®. However, the organization of large-scale vaccination campaigns against HEV may not be particularly cost-effective given the mostly benign course of infection in developing countries and the relatively low incidence in the developed world.

b. Other prophylactic measures

Since HEV is transmitted feco-orally, sanitary measures are probably the most effective strategy available to prevent viral spread. This is especially the case for genotypes 1 and 2 that often occur in large water-borne outbreaks. Availability of clean drinking water and proper disposal of waste water would be effective control strategies. Genotypes 3 and 4 are mostly spread through contaminated

food stuffs, such as the infamous French figatellu sausage made from uncooked pig liver (Berto et al., 2013a; Colson et al., 2010). Thorough heating effectively kills the virus and prevents infection (Feagins et al., 2008a). Although ineffectively, HEV can also be transmitted via blood transfusion (Boxall et al., 2006; Colson et al., 2007), suggesting that screening of donor blood may be warranted. In addition, vertical transmission of HEV has been reported (Khuroo et al., 1995), indicating that extra caution is required in pregnant women.

5. WHY DO WE NEED ANTIVIRAL DRUGS AGAINST HEPATITIS E VIRUS?

a. Current standard of care

Chronic HEV infections in transplant patients can occasionally be resolved by decreasing immunosuppression, leading to spontaneous clearance in about 30% of the patients (Kamar et al., 2011). When this approach is unsuccessful and for other types of patients, there are generally 2 possibilities: the use of pegylated interferon-alpha (PEG-IFN α) or ribavirin. PEG-IFN α has been used successfully in liver transplant, kidney transplant and leukemia patients with chronic hepatitis E (Alric et al., 2010; Haagsma et al., 2010; Kamar et al., 2010a, 2010c). However, ribavirin seems to be the drug of choice in most cases with successful treatments being reported for multiple types of transplant patients (Kamar et al., 2010d; Mallet et al., 2010; Pischke et al., 2013, 2012), but also for HIV and leukemia patients with chronic hepatitis E (Giordani et al., 2013; Neukam et al., 2013). Acute hepatitis E seems to respond to ribavirin treatment as well (Gerolami et al., 2011; Pischke et al., 2013). In addition, the anti-HEV activity of both drugs has been confirmed *in vitro* (Debing et al., 2013a). Nevertheless, they need to be administered for at least 3 months and are known for their severe adverse effects. For PEG-IFN α for instance, this includes influenza-like symptoms and neuropsychiatric side effects (Manns et al., 2006). Ribavirin on the other hand may induce severe anemia necessitating dose reductions (Kamar et al., 2010d; Pischke et al., 2012). These reductions may in turn lead to treatment failure (Pischke et al., 2013). One may deem such severe side effects acceptable in light of the severity of chronic hepatitis E (as is the case for chronic hepatitis C as well), but this is certainly not true when these drugs would be used for prophylaxis or to treat mild

infections. In addition, both ribavirin and PEG-IFN α are contra-indicated in pregnant women and other specific patient populations, leaving no available treatment options for these people. Also when considering acute infections during large outbreaks in developing countries, PEG-IFN α is not an option due to the fact that parenteral administration is needed and the required follow-up of hematological parameters during ribavirin treatment is difficult to implement in such settings.

b. Future therapy for hepatitis E

For the reasons stated above, safe and effective treatments for hepatitis E are urgently required. In case of acute infections, antiviral drugs would be useful to shorten the period of illness and prevent progression to fulminant hepatic failure. Such application would require rapid diagnosis of hepatitis E (see also section 3.c.). Another possibility would be to use antivirals to halt viral spread during epidemics and outbreaks. The fact that these outbreaks occur rather often in refugee camps (e.g. (Ahmed et al., 2013; Centers for Disease Control and Prevention (CDC), 2013)) may represent an opportunity for clinical trials testing the prophylactic potential of HEV inhibitors if such studies would be appropriate from an ethical point-of-view.

In pregnant women, such drugs could be life-saving for both mother and child, on the condition that they are devoid of teratogenic and significant adverse effects. Ideally, these women should be screened regularly with a rapid and sensitive HEV test and treated as soon as possible. This may be difficult to implement in developing countries where genotype 1 is endemic, so an approved HEV inhibitor should be sufficiently potent to arrest an established (fulminant) infection. Modulation of the hormonal system may be another interesting therapeutic option (see suggestions in section 7.f.), although the development of such strategy would require more detailed insights into disease pathogenesis.

For chronically infected patients, rapid clearance of HEV is required before irreversible progression to cirrhosis has occurred. Ideally, these drugs should be applicable in a diverse range of immunocompromised patients without overt toxicity. Since ribavirin treatment has a rather good

efficacy in chronically HEV-infected patients, a combination regimen with another HEV-inhibitor could be envisaged (as is currently being explored for HCV: ribavirin + direct-acting antiviral(s), e.g. (Osinusi et al., 2013; Zeuzem et al., 2013)). This may allow decreasing the ribavirin dosage, thus reducing and hopefully avoiding anemia and other side effects. In addition, we observed a slight synergistic effect *in vitro* for the combination of ribavirin and interferon- α (Debing et al., 2013a), suggesting that such a combination regimen may be worth considering in the clinical setting. Successful combination therapy has already been reported for a chronically HEV-infected HIV patient (Dalton et al., 2011b).

Developing antiviral drugs for the treatment of HEV infections will commercially not be as rewarding as for instance the development of HCV inhibitors (Debing et al., 2013b). Therefore, it appears opportune to consider other strategies than the classical discovery-development of completely new chemical entities as well, for instance off-label use of drugs with robust anti-HEV activity that are registered for unrelated indications when such molecules would be identified.

6. CURRENTLY AVAILABLE METHODS FOR DRUG TESTING

a. *In vitro* testing

Efficient cell culture systems for HEV have only recently become available. The Okamoto research group reported on both genotype 3 and 4 strains that replicate in PLC/PRF/5 (hepatoma) and/or A549 (lung adenocarcinoma) cell lines (Takahashi et al., 2010; Tanaka et al., 2009, 2007). The PLC/PRF/5 cells were also employed in a 3D cell culture system for HEV (Berto et al., 2013b). On the other hand, the NIH research group of Emerson derived a passage 6 virus of the Kernow-C1 strain that replicates in Huh7 and especially HepG2/C3A hepatoma cells (Shukla et al., 2012, 2011). This strain is derived from a chronically infected patient and contains an inserted human ribosomal S17 RNA fragment in the hypervariable region (Shukla et al., 2011). Detailed analyses indicated that this fragment and several additional mutations contributed to the improved *in vitro* replication. Although the replication capacity of this strain is sufficient for virus yield assays (e.g. (Debing et al., 2013a)),

overall growth kinetics are still rather slow. No cytopathic effect (CPE) has been described for any of these HEV strains, precluding the use of standard virology techniques such as CPE reduction assays and plaque assays. In addition, genotype 1 replicates only poorly in cell culture (Nguyen et al., 2013) while it probably accounts for most of the human infections worldwide.

Several replicon constructs have also been established in which the 5' part of the structural proteins is replaced by a GFP, neomycin resistance or luciferase gene (Graff et al., 2006; Shukla et al., 2012). The Kernow-C1 p6/luc reporter replicon proved especially useful in our hands as transient transfection into Huh7 cells allows for a 3-day antiviral assay to be performed (Debing et al., 2013a). For large-scale cell-based screenings with such replicons, a selectable reporter replicon would be highly convenient.

Another possible strategy to identify novel inhibitors of HEV replication is to use a surrogate virus. We recently reported that the cutthroat trout virus (CTV) may serve as such a surrogate (Debing et al., 2013c). CTV was isolated in 1988 from spawning trout in the western USA (Hedrick et al., 1991) and recent studies revealed that the virus belongs to its own genus in the *Hepeviridae* family (Smith et al., 2013). It has a remarkable similarity to HEV, especially when considering the helicase and polymerase sequences (Batts et al., 2011; Debing et al., 2013c). CTV replicates readily in cell culture allowing for RT-qPCR-based virus yield assays to be performed (Debing et al., 2013c). In addition, its *in vitro* replication kinetics can be further improved through repeated passaging (our unpublished results). In addition, CTV is a cytopathic virus. The CPE induced in CHSE-214 cells is rather limited, but we observed that nearly complete CPE can be attained in other piscine cell lines (our unpublished results). The avian HEV has also been successfully employed as a surrogate model (e.g. (Kenney et al., 2012; Pudupakam et al., 2011)).

In conclusion, recent developments have considerably expanded the number of assays and tools available for HEV antiviral studies. However, the possibilities are still rather limited and the field

would benefit from for instance HEV strains with improved replication kinetics, enzymatic assays for the different non-structural proteins and selectable reporter replicons.

b. Evaluation in laboratory animals

An ideal animal model for HEV would be a small inexpensive animal (preferably rodent) that can be infected with human HEV or at least a closely related virus and that develops acute hepatitis with a clear increase in liver markers and with high viral titers. Mortality is not required, although a lethal phenotype is highly useful for antiviral drug testing. An animal model that mimics the hormone-dependent effects observed in pregnant women would be a plus.

Several animal models are available for *in vivo* HEV studies (see table 1 for an overview), but they all have certain limitations. For instance, chicken and trout can be used as experimental animal models when infected with avian HEV and CTV respectively (Billam et al., 2005; Hedrick et al., 1994). Since both viruses are only surrogates for human HEV, further validation of experimental results would be required in another model. Genuine HEV infections can be performed in pigs ((Feagins et al., 2008b; Halbur et al., 2001; Sanford et al., 2011) and non-human primates such as macaques and chimpanzees (Emerson et al., 2001; Meng et al., 1998; Purcell et al., 2003; Yu et al., 2010). , However, ethical concerns as well as practical issues may make such studies complicated. Rodents may present a more accessible model organism. For instance, laboratory rats can be experimentally infected with rat HEV, but contradicting reports have been published for the human HEV genotypes (Li et al., 2013a, 2013b; Purcell et al., 2011; Zhu et al., 2013). Successful infection of Balb/c nude but not C57BL/6 mice with HEV was reported (Huang et al., 2009; Li et al., 2008), while rabbits can be infected with rabbit HEV and certain genotype 4 strains (Cheng et al., 2012). Finally, infection of Mongolian gerbils with genotype 4 has also been reported (Li et al., 2009). Due to the large variability between published results, a robust model that has been evaluated by multiple laboratories has not yet been reported. In addition, none of these models resulted in a lethal phenotype. For the predominant genotype 1 HEV, primates are even the only available model at this time. Promising

strategies towards a robust animal model may be infection of immunodeficient rats or mice with rat HEV, discovery studies for a murine HEV species, HEV infection of mice with chimeric human or porcine livers (Meuleman et al., 2005) or establishment of transgenic mice with a human HEV receptor (when identified), as was done successfully for poliovirus (Ren et al., 1990) and HCV (Dorner et al., 2011).

c. Clinical trials

When a HEV inhibitor would be shown to be successful in a (surrogate) animal model and would have an excellent safety and pharmacokinetic profile, clinical studies would be the next stage in development. For these studies, one could consider treating chronically infected patients, possibly in a combination regimen with ribavirin. However, these patients may have multiple co-morbidities and there could be confounding factors such as concomitant drug use leading to drug-drug interactions. Since hepatitis E has a rather long incubation period and clinical symptoms are often apparent for several weeks, clinical studies could possibly be performed in an outbreak setting as well; in this way, both prophylactic and therapeutic efficacy may be assessed.

7. POTENTIAL DRUG TARGETS

Below we present a selection of viral and host proteins may be attractive targets for antiviral therapy (see also table 2).

a. Inhibitors of HEV entry

The entry of a virus particle into the host cell is a multi-step process that involves attachment of the virus to its receptor on the cellular membrane, internalization of the virion-receptor complex and subsequent uncoating of the viral capsid releasing the RNA genome into the cytoplasm. The functional HEV receptor is still unknown to date, although there are indications that genotype 1 may use a different receptor(s) than genotype 3 (Nguyen et al., 2013). It was also found that HEV attaches to HSPGs, more specifically to 6-O-sulfated syndecan-1, which may account for its liver tropism (Kalia et al., 2009). It is hypothesized that HSPGs act as a highly abundant initial attachment receptor that

binds HEV with relatively low affinity. In a second step, the virion probably transfers to a high-affinity functional receptor and the resulting complex is internalized. Structure determination of a HEV-like particle combined with mutation and cell binding studies have identified a receptor binding site on top of the P2 dimer that protrudes from the 2-fold axis of symmetry (Yamashita et al., 2009). Interestingly, this site is homologous to the norovirus receptor-binding site that attaches to histo-blood group trisaccharides (Guu et al., 2009). In addition, another sialic acid-binding site was found in the P1 region of the capsid protein (Guu et al., 2009).

Despite the limited information that is available on HEV attachment and entry, several potentially interesting antiviral strategies can be derived from these data. First, the homology between the putative HEV and norovirus receptor-binding sites suggests that norovirus attachment inhibitors could possibly be interesting leads for further development into anti-HEV drugs. No confirmed norovirus entry inhibitors have been described to date, but two potentially interesting prototype molecules were designed through NMR binding studies (Rademacher et al., 2011) and in a similar way, citrate was found to compete with histo-blood group saccharides for norovirus binding (Hansman et al., 2012), suggesting a promising role for glycomimetics. A second and possibly overlapping approach is to search for inhibitors of HEV attachment to HSPGs. Heparan sulphate and related molecules inhibit the attachment of multiple viruses, both *in vitro* and *in vivo* (e.g. (Ali et al., 2012; Bugatti et al., 2007; Lee et al., 2006)). However, the clinical applicability of such molecules remains questionable and would require complete abolishment of any anticoagulative properties. Pentosan polysulphate is such an oligosaccharide derivative that is approved and marketed for pain relief in interstitial cystitis (Davis et al., 2008). Given that this drug inhibits entry of multiple viruses (Baba et al., 1988; García-Villalón and Gil-Fernández, 1991), it may be worthwhile to test it as a therapeutic option for hepatitis E, although it still has some anticoagulant properties (Scully et al., 1983). Thirdly, it has been shown that a truncated ORF2 protein is capable of preventing HEV infection *in vitro* (He et al., 2008). Through further truncation of this protein or otherwise mimicking the receptor-binding region of HEV, it would theoretically be possible to prevent virions from binding

to their cellular receptor. To illustrate the feasibility of such an approach, we refer to Myrcludex-B which is a lipopeptide derived from the HBV envelope protein and efficiently inhibits HBV entry *in vitro* and *in vivo* (Volz et al., 2013).

The strategies outlined above illustrate that the lacking of an identified receptor is an important hurdle for the identification and study of attachment, entry and uncoating inhibitors for HEV. Now that efficient cell culture systems are available (e.g. (Shukla et al., 2012)), this hiatus can and should be addressed.

b. RNA-dependent RNA polymerase inhibitors

Following release of the viral RNA in the cytoplasm and initial translation, the RNA genome is replicated by an RNA-dependent RNA polymerase. Sequence alignments predicted an RdRp-encoding sequence at the 3' end of ORF1 (see figure 1, (Koonin et al., 1992)) that belongs to the alphavirus-supergroup of RdRp's (Koonin, 1991). The polymerase activity was later confirmed by detection of newly synthesized negative-sense viral RNA *in vitro* (Agrawal et al., 2001; Rehman et al., 2008). The RdRp interacts with stem loops in the 3' end of the viral genome and with the polyA-tail (Agrawal et al., 2001) and co-localizes with the endoplasmatic reticulum (Rehman et al., 2008). However, further details about the HEV RdRp structure and function are missing.

As evidenced by the success of nucleoside and nucleotide inhibitors of HIV and herpesviruses, viral polymerases are attractive targets for antiviral therapy. Also the RdRp of RNA viruses has been targeted successfully by such molecules, consider for instance the nucleoside analogues that were developed against HCV, e.g. sofosbuvir is highly active, safe and has a high barrier to resistance. Sofosbuvir has successfully completed phase 3 clinical trials (Lawitz et al., 2013) and may receive market approval in the near future. 2'-C-methylcytidine (2'CMC) is a related molecule and was the first nucleoside analogue that entered clinical studies for the treatment of HCV infections. It has been shown to *in vitro* inhibit the replication of a number of other positive-sense single-stranded RNA viruses (Julander et al., 2010; Rocha-Pereira et al., 2013). However, neither 2'CMC nor a number of

its analogues exhibited significant activity in the transient HEV replicon assay (as described in (Debing et al., 2013a), unpublished results). Also only moderate antiviral activity of 2'CMC was observed against CTV (Debing et al., 2013c). Despite these negative results, other nucleos(t)ide analogues may possibly be interesting inhibitors of HEV replication. Moreover, research efforts could be directed towards developing an RdRp inhibitor that targets both HEV and the distantly related alphavirus family. Such a broad-spectrum inhibitor would provide a much-needed treatment option for multiple infections by neglected viruses such as the Chikungunya virus, Sindbis virus and the equine encephalitis viruses. Elucidation of the HEV RdRp crystal structure and development of a convenient enzymatic assay would allow to jumpstart this specific domain of HEV antiviral research.

c. Methyltransferase inhibitors

The HEV genome has a 5' cap structure which is a crucial requirement for infectivity (Emerson et al., 2001). Capping is a multistep process involving hydrolysis of the γ -phosphate from the terminal nucleotide, subsequent conjugation to GMP resulting in a 5'-ppp-5' triphosphate bond and finally methylation of the newly added guanosine. The 5' proportion of the ORF1 sequence was predicted to encode a viral methyltransferase (Koonin et al., 1992) and indeed, the expressed protein displays guanylyltransferase and guanine-7-methyltransferase activities (Magden et al., 2001). The missing RNA triphosphatase function may be fulfilled by the HEV helicase (Karpe and Lole, 2010a).

Since HEV is heavily dependent on the capping of its RNA genome for infectivity, the viral methyltransferase seems an ideal target for antiviral therapy, all the more since these enzymatic activities are virus-specific (Magden et al., 2001) and thus may allow for development of selective inhibitors. Successful targeting of viral methyltransferases has been described for instance for dengue virus (Barral et al., 2013) and West Nile virus (Chen et al., 2013). Moreover, a highly efficient inhibitor of Chikungunya virus replication that selects for resistance mutations in nsP1 (viral methyltransferase) was recently identified in our laboratory (unpublished results; Delang L., Leyssen P. & Neyts J.); indicating that inhibition of this transferase may be a valuable strategy to inhibit the

replication of RNA viruses, including HEV. Solving the crystal structure and development of robust enzymatic assays would be significant advances.

d. Helicase inhibitors

RNA viruses require the RNA-unwinding activity of a virally encoded helicase enzyme for replication; the energy needed for this process is provided by the hydrolysis of NTPs (Kwong et al., 2005). As for the RdRp and methyltransferase, the NTPase and RNA unwinding activities of the predicted HEV helicase domain have been confirmed *in vitro* (Karpe and Lole, 2010b). This helicase belongs to the 5'-to-3' unwinding SF-1 helicase superfamily, which also comprises the alphavirus and coronavirus (CoV) helicases. Potent inhibitors have been identified for the SARS-CoV nsP13 helicase (Adedeji et al., 2012; Tanner et al., 2005), suggesting that it may also be possible to develop inhibitors of the HEV helicase. An important caveat is that such inhibitors need to be highly specific for viral helicases without affecting host helicase activity to avoid toxicity. Examples from the herpesvirus field (helicase-primase inhibitors such as Ietermovir which has successfully finished phase 2 clinical studies (Marschall et al., 2012)) show that such selectivity can be attained.

e. Targeting other viral proteins

Besides the above mentioned enzymes, the HEV genome encodes several other proteins of which the function and significance have not been elucidated completely, like the macro domain, the viral protease and the ORF3 protein. Given that more information would become available, they may constitute suitable targets for antiviral therapy.

The macrodomain, formerly known as the X-domain, is located just upstream of the helicase gene (figure 1, (Koonin et al., 1992)). Its name is derived from the homologous non-histone domain of the macroH2A histone (Egloff et al., 2006). The exact function of the HEV macrodomain is unclear, although it strongly binds poly(ADP-ribose) (Egloff et al., 2006), an important post-translational protein modification involved in cell survival and apoptosis, among other functions (Schreiber et al., 2006). Since it has been suggested that the biological function of viral macrodomains may be

unrelated to that of their human homologs (Neuvonen and Ahola, 2009), they could represent attractive targets for inhibition. However, this would require a more profound understanding of the function and activity of this domain.

Secondly, a papain-like cysteine protease domain has been predicted in the HEV genome sequence (Koonin et al., 1992), but it remains unclear whether this protease is fully functional. Consequently, one of the enigmas of HEV molecular biology is whether ORF1 is processed into discrete functional units or not: several publications reported processing of ORF1 to some extent (Panda et al., 2000; Parvez, 2013; Ropp et al., 2000; Sehgal et al., 2006), while others found no processing whatsoever (Ansari et al., 2000; Perttälä et al., 2013; Suppiah et al., 2011). On the other hand, deubiquitination activity has been reported for the methyltransferase-protease fusion domain which may be involved in combating cellular antiviral responses (Karpe and Lole, 2011) and a recent mutational study suggested a glycine-triad as the protease substrate sequence (Parvez, 2013). Although viral proteases in general are interesting targets for antiviral therapy (as exemplified in the fields of HIV and HCV), more insight into the activity, function and structure of the HEV protease would be essential before focusing on protease inhibitors.

ORF3 encodes a 114aa phosphoprotein (Graff et al., 2006) that is exclusively found in hepeviruses. ORF3 protein is dispensable for *in vitro* infection of cultured cells (Emerson et al., 2006), but required for infection and seroconversion of rhesus macaques (Graff et al., 2005). A number of functions have been proposed and several binding partners have been identified (Holla et al., 2013; Ratra et al., 2008), but in general, ORF3 protein seems to optimize the host cell for HEV replication by increasing cell survival (Chandra et al., 2010, 2008; Moin et al., 2007) and suppressing interferon- α signaling (Dong et al., 2012). In addition, ORF3 protein has been implicated in virion egress (Yamada et al., 2009) and disruption of blood coagulation (Geng et al., 2013). It should be noted that most of these results have been obtained in artificial systems, i.e. overexpression of ORF3 protein in cultured cells instead of genuine infection with HEV. In order to be targeted for antiviral development, more

insight into the ORF3 structure and function is required. Since the protein has multiple cellular binding partners, it may be interesting to look for inhibitors of these protein-protein interactions (see also section 7.f.). Such an approach may yield very specific inhibitors of HEV replication with low toxicity and a high barrier to resistance, especially given the overlap with ORF2 which is expected to substantially limit the number of viable mutations. The feasibility of identifying protein-protein interaction inhibitors as antiviral molecules was proven for the interaction between LEDGF/p75 and the HIV integrase for instance (Christ et al., 2010).

f. Host factors

Since many direct-acting antiviral agents are prone to the emergence and selection of resistant viruses, there is an increasing interest in targeting host factors that are co-opted by viruses for their own replication. Such host factor-targeting antivirals should have an increased barrier to resistance and may potentially have broad-spectrum activity. Multiple binding partners have been identified for HEV structural and non-structural proteins. The functional significance of many of these interactions remains unclear to date, but some of the host factors may be well-suited for antiviral targeting. Here, we discuss a few host factors that we believe have the most potential at being druggable.

First, tumor susceptibility gene 101 (Tsg101) is a central mediator in the endosomal protein sorting pathway (Surjit et al., 2006). HEV ORF3 protein has a PSAP-motif through which it associates with Tsg101, thus increasing secretion of the immunosuppressive α 1-microglobulin and locally suppressing the host immune response (Surjit et al., 2006). In addition, Tsg101 is required for virion release by interacting with the ORF3 protein PSAP-motif (Kenney et al., 2012; Nagashima et al., 2011a, 2011b). The involvement of Tsg101 in virion release is not limited to HEV; it was also found to be essential for HIV and Ebola virus budding (Garrus et al., 2001; Martin-Serrano et al., 2001) and is being explored as a target for antiviral therapy (Chen et al., 2010). For instance, cyclic peptides blocking the interaction between Tsg101 and the PTAP motif of the HIV Gag-protein were found to block HIV budding (Tavassoli et al., 2008). Moreover, Tsg101 is expressed on the cell membrane

during both HIV and influenza virus infection and targeting by antibodies blocks virus production (Bonavia et al., 2010; Diaz et al., 2010). Similar questions can be posed for HEV: does HEV induce expression of Tsg101 at the cell membrane? Can the interaction between Tsg101 and ORF3 be blocked with a small molecule or (cyclic) peptide? Potentially, antiviral research on HEV could piggy-back on the ongoing efforts for HIV and influenza virus and thus advance rapidly.

Another interesting finding is that the proteasome inhibitor MG132 inhibits HEV replication, indicating that HEV likely requires an active ubiquitin-proteasome system for infection (Karpe and Meng, 2012). Similar findings have been reported for influenza virus (Haasbach et al., 2011), HIV (Schubert et al., 2000) and vaccinia virus (Satheshkumar et al., 2009). This suggests that targeting the proteasome system may be an interesting strategy for identifying broad-spectrum antiviral drugs. Proteasome inhibitors such as bortezomib and carfilzomib are currently being used in the treatment of multiple myeloma, based on the increased susceptibility of cancer cells compared to non-malignant cells (Hideshima et al., 2001). However, it is unknown whether such a selectivity can also be attained for virus-infected cells versus healthy cells to avoid severe side effects.

A similar analysis may apply to heat shock protein 90 (hsp90) as a cellular target for anti-HEV drugs and antiviral therapy in general. Hsp90 is required for intracellular trafficking of HEV particles and inhibition of hsp90 with geldanamycin blocks HEV infection (Zheng et al., 2010). Many viruses depend on hsp90 and their replication can be blocked by hsp90 inhibitors (Basha et al., 2005; Geller et al., 2013; Sun et al., 2013). Such inhibitors are currently being developed as anticancer therapies ((Jhaveri and Modi, 2012) for an overview), but the question remains if sufficient selectivity can be attained for safe antiviral therapy. An alternative strategy may be to specifically inhibit the protein-protein interaction between the HEV capsid and hsp90, thus leaving hsp90 enzymatic activity undisturbed.

Finally, there are multiple indications that HEV replication may be influenced by sex hormones. First, mortality increases dramatically in pregnant women infected with genotype 1 (up to 25%, (Khuroo et

al., 1981; Tsega et al., 1993)). The underlying mechanism is still unclear, but it is known that low progesterone receptor mRNA levels and mutations in the progesterone receptor gene (PROGINS) are associated with poor pregnancy outcome (fulminant hepatic failure, fetal and maternal death) during HEV infection (Bose et al., 2011). On the other hand, autochthonous HEV infections in developed countries seem to primarily affect males over 50 (Dalton et al., 2011a; Davern et al., 2011; Mansuy et al., 2009). We reported that the replication of the CTV, a HEV surrogate virus, can be directly influenced by different concentrations of progesterone, testosterone and 17 β -estradiol (Debing et al., 2013c), suggesting the possibility of a similar phenomenon in HEV infection. Several potential strategies can be derived from the limited information that is available. Since decreased progesterone receptor activity is associated with poor pregnancy outcome in hepatitis E (Bose et al., 2011) and high concentrations of progesterone inhibit CTV replication (Debing et al., 2013c), one may consider progesterone supplementation in pregnant women with hepatitis E. Such supplementation has been approved by the FDA for the prevention of preterm birth (Norwitz and Caughey, 2011). Similarly, testosterone levels decrease with age and low testosterone concentrations facilitate CTV replication (Debing et al., 2013c), suggesting that testosterone supplementation may be beneficial in elderly man (chronically) infected with HEV. A third possibility may be the use of selective estrogen receptor modulators (SERMs), such as tamoxifen and raloxifene. SERMs were found to inhibit HCV replication *in vitro* (Murakami et al., 2013; Watashi et al., 2007) and raloxifene improved the efficacy of pegylated interferon + ribavirin in menopausal women chronically infected with HCV (Furusyo et al., 2012). It would be interesting to look into the effects of SERMs on HEV or CTV replication as they may represent another possible treatment option for hepatitis E (but not during pregnancy). To fully explore the potential treatment of hepatitis E through modulation of the hormonal system, a robust animal model displaying hormone-dependent virus replication would be much appreciated.

8. DIRECTIONS FOR FUTURE RESEARCH

Antiviral drugs for the treatment of hepatitis E are required for both acute and chronic infections. Such drugs should have an increased potency, efficacy and safety compared to the currently used

ribavirin and PEG-IFN α , thus allowing for prophylactic use, containment of outbreaks and preferably treatment of pregnant women and other high-risk patients as well. It would also be interesting to further characterize the mechanism of action of ribavirin and PEG-IFN α in hepatitis E. As evident from the discussion above, HEV is an understudied pathogen and most of the suggested antiviral strategies require a more elaborate fundamental knowledge of the molecular virology. In addition, better model systems should be developed, both *in vitro* and *in vivo*, for proper antiviral research to be conducted.

HEV is an extremely interesting pathogen that deserves more profound study. In the last decade, much effort has gone to the HCV antiviral field. As many (candidate) drugs are currently in advanced clinical development, awaiting market approval or even on the market, HEV research could potentially benefit from research groups switching their main focus from HCV to HEV.

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 1072

FIGURE LEGENDS

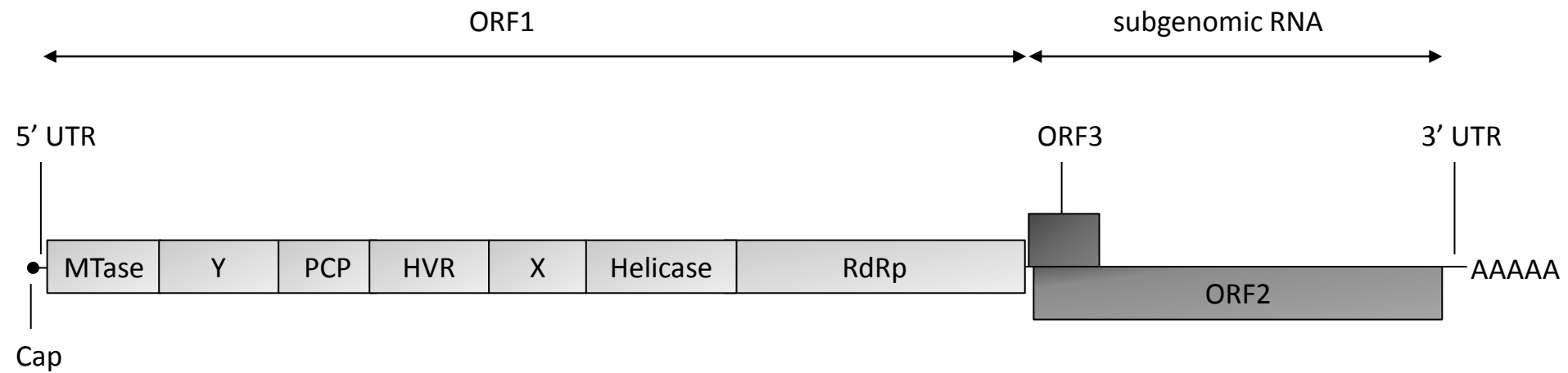
Figure 1 – Organization of the HEV genome: Non-structural proteins are translated from ORF1 while the ORF2 and ORF3 structural proteins are translated from a single subgenomic RNA. UTR, untranslated region; Y, Y-domain; PCP, papain-like cysteine protease; HVR, hypervariable region; X, macro domain; RdRp, RNA-dependent RNA polymerase.

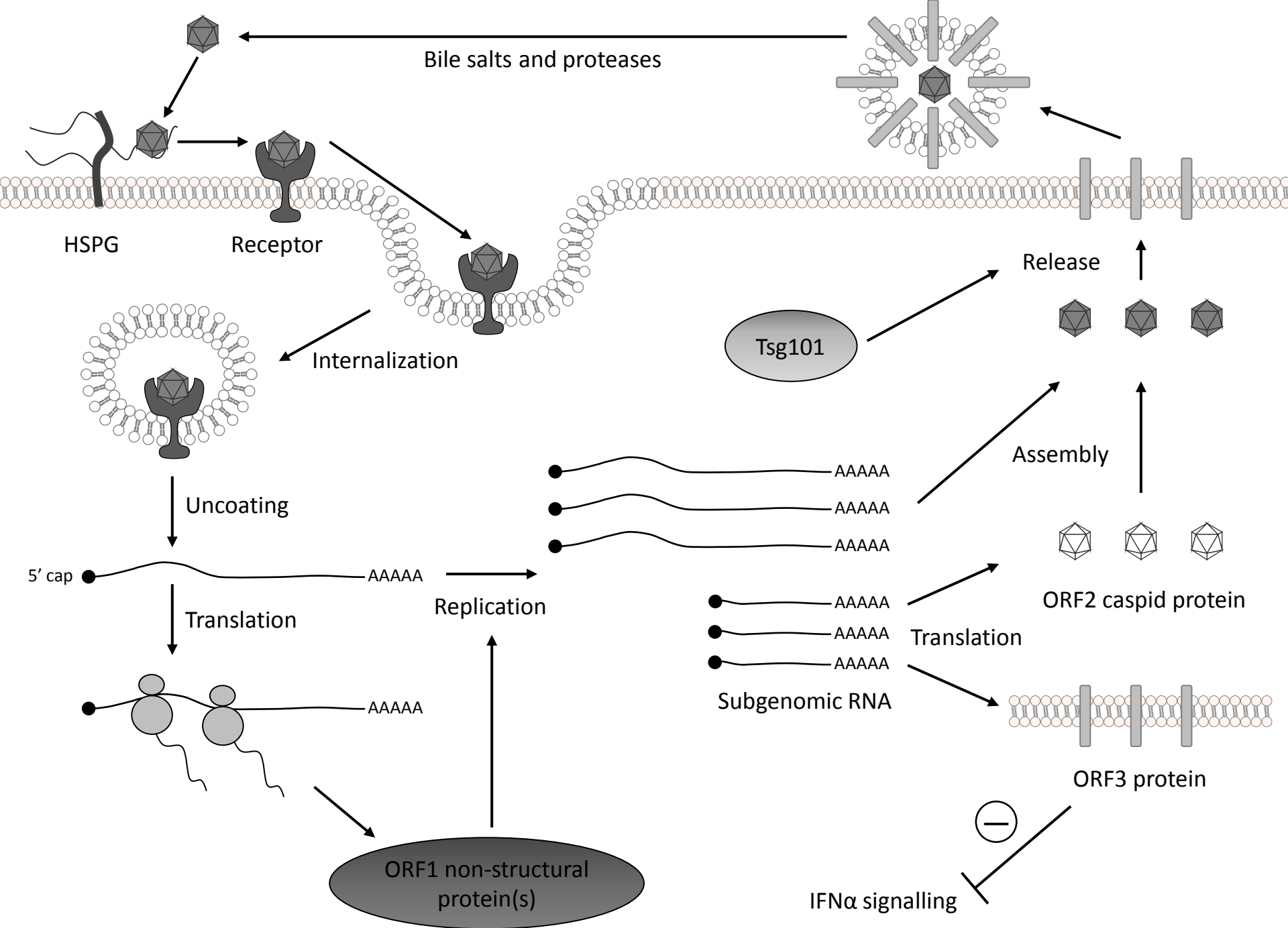
Figure 2 – HEV replication cycle: HEV particles first bind to heparan sulphate proteoglycans (HSPG) and are consequently transferred to an unknown functional receptor, thus mediating cellular uptake through clathrin-mediated endocytosis. Following uncoating, the viral RNA genome is released into the cytoplasm and translated into non-structural proteins. These proteins form a replication complex that produces new full-length and subgenomic viral RNA. The latter is translated into capsid protein (ORF2) and the membrane associated ORF3 protein that is known to interfere with interferon- α signaling. Viral RNA is packaged into capsid protein and released from the cell with help of the host factor Tumor susceptibility gene 101 (Tsg101). The released particles are associated with lipids and ORF3 proteins; both are consequently removed through the bile acids and digestive proteases respectively.

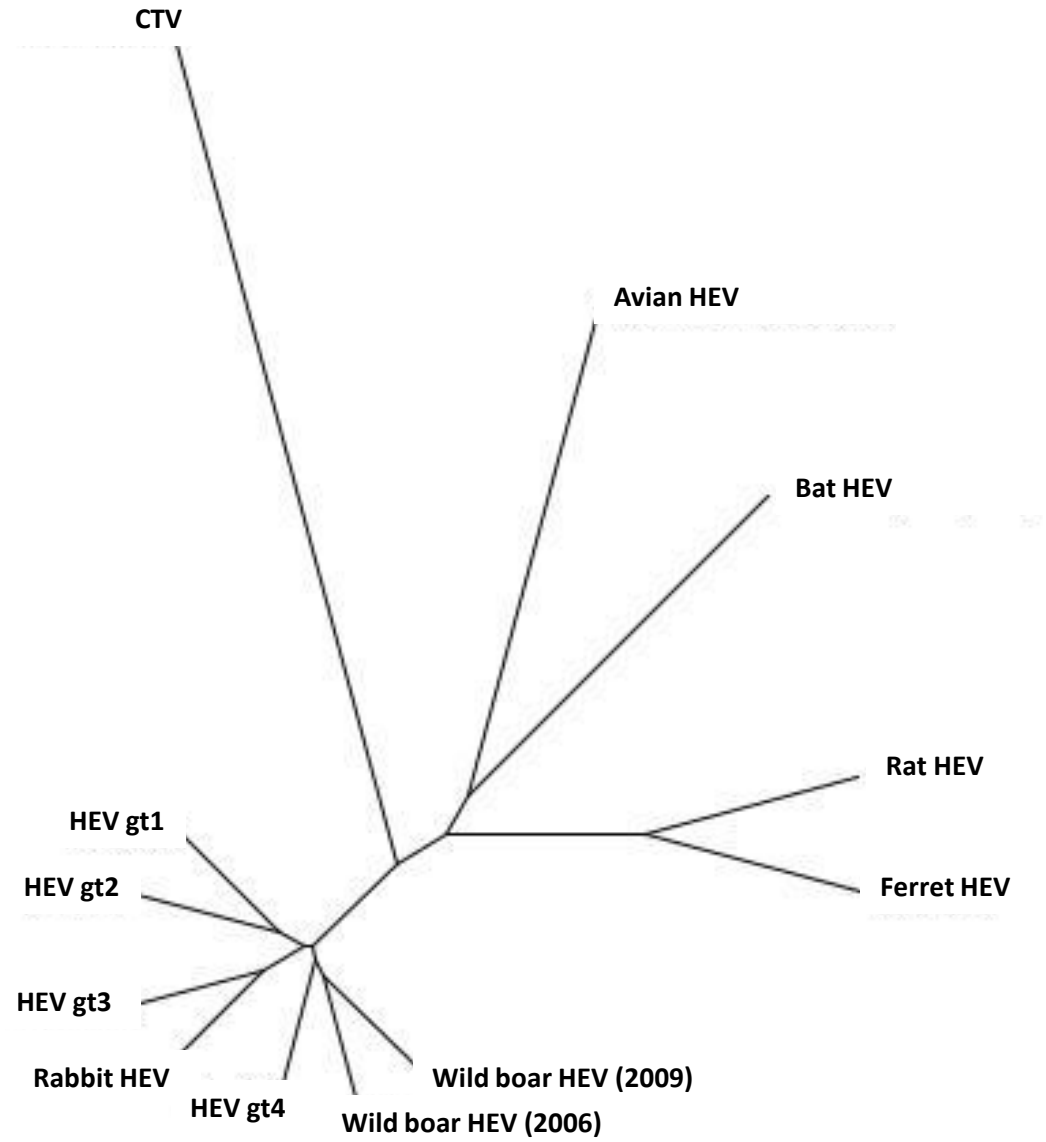
Figure 3 – HEV species and genotypes: The phylogenetic relationship of different human HEV genotypes and the reported animal strains was plotted with the Virus Pathogen Database and Analysis Resource (ViPR, (Pickett et al., 2012)) based on following sequences: HEV gt1 (GenBank accession no. M80581), HEV gt2 (M74506), HEV gt3 (HQ389543), rabbit HEV (FJ906895), HEV gt4 (AB220973), wild boar HEV 2006 (AB602441), wild boar HEV 2009 (AB573435), ferret HEV (JN998606), rat HEV (GU345043), bat HEV (JQ001749), avian HEV (AY535004), CTV (HQ731075). CTV, cutthroat trout virus; gt, genotype.

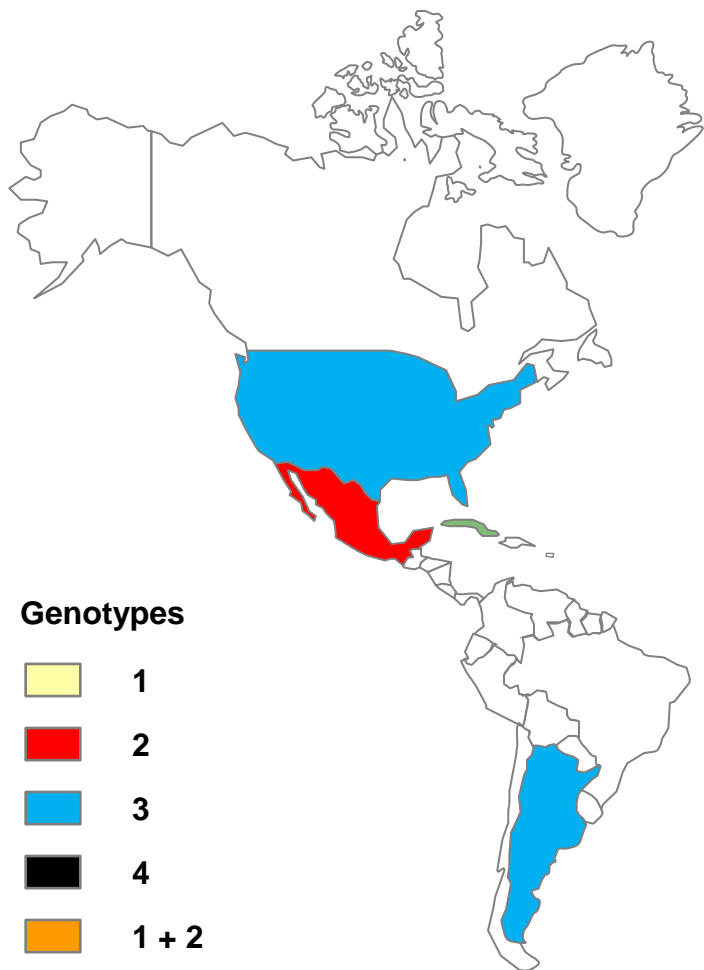
Figure 4 – Geographic distribution of HEV genotypes 1-4: Countries with confirmed human infections are color-coded according to the detected genotype. This is probably an incomplete

1097 picture as there are no data available for many countries and genotyping is not always performed
1098 and/or reported.

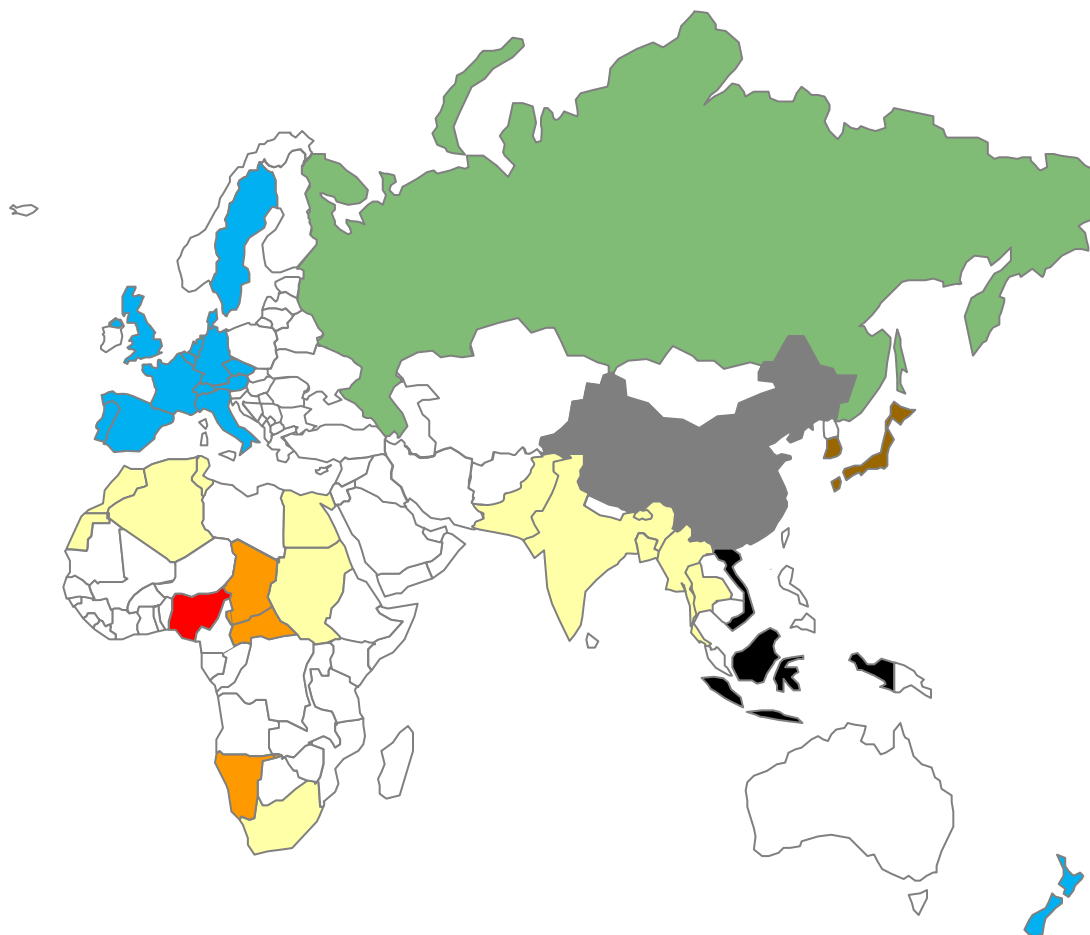
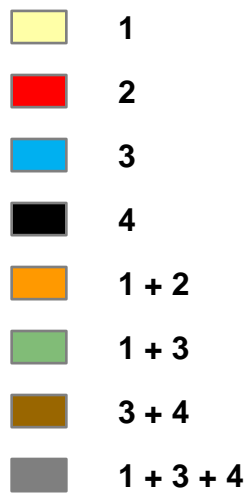








Genotypes



Animal model	Virus species	Characteristics	References
Chicken	Avian HEV	Seroconversion, virus shedding, gross hepatic lesions, splenomegaly	(Billam et al., 2005)
Trout	Cutthroat trout virus	Avirulent, only detected during spawning, IFN induction	(Hedrick et al., 1994)
Pig	HEV gt 3 and 4	Seroconversion, virus shedding, histopathological damage	(Feagins et al., 2008; Halbur et al., 2001; Sanford et al., 2011)
Macaque (rhesus, cynomolgus), chimpanzee	HEV gt 1-4	Seroconversion, virus shedding, histopathological damage	(Emerson et al., 2001; Meng et al., 1998; Purcell et al., 2003; Yu et al., 2010)
Rat (Wistar)	Rat HEV	Seroconversion, virus shedding, no alterations in ALT	(Li et al., 2013b)
	HEV gt 1, 3 or 4	Not infectable	(Li et al., 2013b)
(Nude)	Rat HEV	Seroconversion, limited virus shedding, higher titers than in immunocompetent rats	(Li et al., 2013b; Purcell et al., 2011)
	HEV gt 3	Not infectable	(Li et al., 2013a)
(Sprague-Dawley)	Rat HEV	Seroconversion, limited virus shedding, histopathological damage, no alterations in ALT	(Purcell et al., 2011)
	HEV gt 1, 2 or 3	Not infectable (after intravenous injection)	(Purcell et al., 2011)
	HEV gt 4	Seroconversion, virus shedding (after intrahepatic RNA inoculation)	(Zhu et al., 2013)
Mouse (Balb/c nude)	HEV gt 4	Seroconversion, virus shedding, histopathological liver damage	(Huang et al., 2009)
(C57BL/6)	HEV gt 1, 3 and 4	Not infectable	(Li et al., 2008)
Rabbit	Rabbit HEV	Seroconversion, virus shedding	(Cheng et al., 2012)
	HEV gt 4	Seroconversion, virus shedding, symptomatic hepatitis (only for H4-NJ703 strain)	(Cheng et al., 2012)
Mongolian gerbil	HEV gt 4	Virus shedding, slight histopathological liver changes	(Li et al., 2009)

Table 1 – Overview of reported animal models for HEV and surrogate viruses with reported pathology (gt, genotype; IFN, interferon; ALT, alanine transaminase)

HEV-encoded proteins	Confirmed functions	Crystal structure?	References
ORF1	Non-structural proteins		
Methyltransferase	Guanylttransferase, guanine-7-methyltransferase	No	(Magden et al., 2001)
Papain-like cystein protease	Proteolytic processing of ORF1? Deubiquitinating activity	No	(Karpe and Lole, 2011; Parvez, 2013; Perttilä et al., 2013; Sehgal et al., 2006)
Hypervariable region	Influences efficiency of viral RNA replication, host/cell type specificity?	No	(Pudupakam et al., 2011; Shukla et al., 2012)
Macrodomain	Poly-ADP-ribose-binding, weak ADP-ribose 1''-phosphohydrolase activity	No	(Egloff et al., 2006)
Helicase	5'-3' RNA unwinding, NTPase, RNA 5'-triphosphatase	No	(Karpe and Lole, 2010a, 2010b)
RdRp	RNA-dependent RNA polymerase activity	No	(Agrawal et al., 2001; Rehman et al., 2008)
ORF2	Capsid protein	Yes (HEV-like particle)	(Guu et al., 2009; Yamashita et al., 2009)
ORF3	Interaction with multiple cellular proteins, including Tsg101, hemopexin,... Suppression of interferon- α signaling Particle egress	No	(Geng et al., 2013; Ratra et al., 2008; Surjit et al., 2006) (Dong et al., 2012) (Yamada et al., 2009)

Table 2 – HEV-encoded proteins and their (putative) functions